

ABSTRACT

It is intended to efficiently determine a base sequence specifically appearing in an expression gene. For this, providing that the expression gene consists of exons (301)...(306) and especially that exon (301) is united with exon (302) and exon (302) with exon (303), an aggregate of base sequences (401) (403) being a union of exon base sequences (301)...(305) and a boundary base sequence obtained by uniting together base sequences(404) and (405) and base sequences (406) and (407) respectively existing over boundaries between exon (301) and exon (302) and between exon (302) and exon (303) is formed, and the aggregate is searched. If a base sequence is one specifically appearing in the expression gene, the number of search results is 1 and otherwise, the number is plural.